

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/319,831DATE: 05/26/95
TIME: 10:57:39

INPUT SET: S3895.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Hewick, Rodney M.
6 Wang, Jack H.
7 Wozney, John M.
8 Celeste, Anthony J.
9
10 (ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
11
12 (iii) NUMBER OF SEQUENCES: 15
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
16 (B) STREET: 87 CambridgePark Drive
17 (C) CITY: Cambridge
18 (D) STATE: MA
19 (E) COUNTRY: USA
20 (F) ZIP: 02140
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 08/319,831
30 (B) FILING DATE: 6-OCT-1994
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Kapinos, Ellen J.
35 (B) REGISTRATION NUMBER: 32,245
36 (C) REFERENCE/DOCKET NUMBER: GI 5182A-DIV
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 617-876-1170
40 (B) TELEFAX: 617-876-5851
41
42 (2) INFORMATION FOR SEQ ID NO:1:
43
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 23 amino acids
46 (B) TYPE: amino acid

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47 (C) STRANDEDNESS: single
48 (D) TOPOLOGY: unknown
49
50 (ii) MOLECULE TYPE: peptide
51
52 (iii) HYPOTHETICAL: NO
53
54 (iv) ANTI-SENSE: NO
55
56 (vi) ORIGINAL SOURCE:
57 (F) TISSUE TYPE: Bone
58
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
60
61 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
62 1 5 10 15
63
64 Val Ile Ala Pro Gln Gly Tyr
65 20
66
67 (2) INFORMATION FOR SEQ ID NO:2:
68
69 (i) SEQUENCE CHARACTERISTICS:
70 (A) LENGTH: 18 amino acids
71 (B) TYPE: amino acid
72 (C) STRANDEDNESS: single
73 (D) TOPOLOGY: unknown
74
75 (ii) MOLECULE TYPE: peptide
76
77 (iii) HYPOTHETICAL: NO
78
79 (iv) ANTI-SENSE: NO
80
81 (v) FRAGMENT TYPE: internal
82
83 (vi) ORIGINAL SOURCE:
84 (A) ORGANISM: Bos taurus
85 (F) TISSUE TYPE: Bone
86
87
88 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
89
90 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
91 1 5 10 15
92
93 Leu Arg
94
95
96 (2) INFORMATION FOR SEQ ID NO:3:
97
98 (i) SEQUENCE CHARACTERISTICS:
99 (A) LENGTH: 7 amino acids

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100 (B) TYPE: amino acid
101 (C) STRANDEDNESS: single
102 (D) TOPOLOGY: unknown
103
104 (ii) MOLECULE TYPE: peptide
105
106 (iii) HYPOTHETICAL: NO
107
108 (iv) ANTI-SENSE: NO
109
110 (vi) ORIGINAL SOURCE:
111 (A) ORGANISM: Bos taurus
112 (F) TISSUE TYPE: Bone
113
114
115 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
116
117 Ala Cys Cys Ala Pro Thr Lys
118 1 5
119
120 (2) INFORMATION FOR SEQ ID NO:4:
121
122 (i) SEQUENCE CHARACTERISTICS:
123 (A) LENGTH: 23 amino acids
124 (B) TYPE: amino acid
125 (C) STRANDEDNESS: single
126 (D) TOPOLOGY: unknown
127
128 (ii) MOLECULE TYPE: peptide
129
130 (iii) HYPOTHETICAL: NO
131
132 (vi) ORIGINAL SOURCE:
133 (A) ORGANISM: Bos taurus
134 (F) TISSUE TYPE: Bone
135
136
137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
138
139 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
140 1 5 10 15
141
142 Val His Gly Ser His Gly Arg
143 20
144
145 (2) INFORMATION FOR SEQ ID NO:5:
146
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 80 base pairs
149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: double
151 (D) TOPOLOGY: linear
152

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153 (ii) MOLECULE TYPE: DNA (genomic)
154
155 (iii) HYPOTHETICAL: NO
156
157 (iv) ANTI-SENSE: NO
158
159 (vi) ORIGINAL SOURCE:
160 (A) ORGANISM: Bos taurus
161
162 (vii) IMMEDIATE SOURCE:
163 (B) CLONE: acc30
164
165 (viii) POSITION IN GENOME:
166 (C) UNITS: bp
167
168 (ix) FEATURE:
169 (A) NAME/KEY: CDS
170 (B) LOCATION: 25..57
171
172
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
176 Lys Leu Ser Ala Thr Ser Val Leu Tyr
177 1 5
178
179 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80
180 Tyr Asp
181 10
182
183
184 (2) INFORMATION FOR SEQ ID NO:6:
185
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 11 amino acids
188 (B) TYPE: amino acid
189 (D) TOPOLOGY: linear
190
191 (ii) MOLECULE TYPE: protein
192
193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
194
195 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
196 1 5 10
197
198 (2) INFORMATION FOR SEQ ID NO:7:
199
200 (i) SEQUENCE CHARACTERISTICS:
201 (A) LENGTH: 199 base pairs
202 (B) TYPE: nucleic acid
203 (C) STRANDEDNESS: double
204 (D) TOPOLOGY: linear
205

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206 (ii) MOLECULE TYPE: DNA (genomic)

207

208 (iii) HYPOTHETICAL: NO

209

210 (vi) ORIGINAL SOURCE:

211 (A) ORGANISM: Bos taurus

212

213 (vii) IMMEDIATE SOURCE:

214 (A) LIBRARY: Bovine genomic

215 (B) CLONE: Lambda 9800-10

216

217 (viii) POSITION IN GENOME:

218 (C) UNITS: bp

219

220 (ix) FEATURE:

221 (A) NAME/KEY: exon

222 (B) LOCATION: 30..199

223

224 (ix) FEATURE:

225 (A) NAME/KEY: intron

226 (B) LOCATION: 1..29

227

228 (ix) FEATURE:

229 (A) NAME/KEY: CDS

230 (B) LOCATION: 30..179

231

232

233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

234

235 TGCCCGCTGC CCCCTCCCGC CCCC GCCAG GTG CAC CTG CTG AAG CCG CAC GCG 53

236 Val His Leu Leu Lys Pro His Ala

237 1 5

238

239 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101

240 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val

241 10 15 20

242

243 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149

244 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn

245 25 30 35 40

246

247 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 196

248 Met Val Val Arg Ala Cys Gly Cys His

249 45 50

250

251 CAG 199

252

253

254 (2) INFORMATION FOR SEQ ID NO:8:

255

256 (i) SEQUENCE CHARACTERISTICS:

257 (A) LENGTH: 49 amino acids

258 (B) TYPE: amino acid